

Fig. 1

TGGTTGTCCTGGAACTCACTCTGTAGACCAGGCTGGCCATGAACTCACAGA GATCTACCTCCTGAGTGCTGGGATTAAAGGTTTGTGCCACCACCTCCCAAC TCTAAGGTGTTTCTTTAAGTTAGGGGCATAGTAAACATTGTTGAGATACTA GAGGAACACTGAATGAAAATTTGGACATCTCTGCTTTAGGTTTGTGCTGAG CAGTTTGCCTCTTATCTTCACCTATGCTGAAAAGTTTGAGTTCATAATTTTG **ATGAACTTACCTTTAAAATGTCAGTAACAACTCTGCATGGTTTTCTTCTTAC** CTCCATAGGTATGGTCTGAATATGCGTTGTTTGGCAGCTCGGGTCAACTAT **AAGACTTTGATTATCATCTGTGCGCTATTCACTTTTGGTCACAGTACTTTTGT GGAATAAGTGTTCCAGCGACAAAGCAATCCAGTTTCCTCGGCACTTGAGTA GTGGATTCAGAGTGGATGGATTAGAAAAAAGATCAGCAGCATCTGAAAGTA ACCACTATGCCAACCACATAGCCAAACAGCAGTCAGAAGAGGCATTTCCTC** AGGAACAACAGAAGGCACCCCCTGTTGTTGGGGGCTTCAATAGCAACGGG **GGAAGCAAGGTGTTAGGGCTCAAATATGAAGAGATTGACTGTCTCATAAAC** TTCACTTGGGTAGAGAAATACTTTG<u>ATGTTTATGGAAAAGTGGTCCGAGTA</u> TGACGCTATGATCGATTTGAATTC::TCTCATAGCTATTCCAAAGTCTATGCA CAGAGAGCCCCTTATCACCCTGATGGTGTTTTATGTCCTTTGAAGGCTACAATG TGGAAGTCCGAGACAGAGTCAAGTGCATAAGTGGGGTTGAAGGTGTACCTTTAT CTACACAGTGGGGACCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATG GGTTAAGTCACTACAGCAAGAATCTAACTGAAAAACCCCCTCATATAGAGGTAT ATGAAACAGCAGAAGACAGGGACAAAAACAGCAAGCCCAATGACTGGACTGTG CCCAAGGGCTGCTTTATGGCTAGTGTGGCTGATAAGTCAAGATTCACCAATGTT AAACAGTTCATTGCTCCAGAAACCAGTGAAGGTGTATCCTTGCAACTGGGGAAC **ACAAAAGATTTTATTTCATTTGACCTCAAGTTCTTAACAAATGGAAGCGTGT** <u>CTGTGGTTCTGGAGACGACAGAAAAGAATCAGCTCTTCACTGTACATTATGTCT</u> CAAATACCCAGCTAATTGCTTTTAAAGAAAGAGACATATACTATGGCATCGGGC CCAGAACATCATGGAGCACAGTTACCCGGGACCTGGTCACTGACCTCAGGAAA GGAGTGGGTCTTTCCAACACAAAAGCTGTCAAGCCAACAAGAATAATGCCCAA

TRATE TRADEN

> FIGURE 1 CONTINUED



| 1 M | 1 MSKYLSSQRDALSAPAL-PVSRENREPPKFQGVKQREPIVFFINRINIKAVILIVIC-ALFTILVTVI-L 1 MVIVSIKPFNIFSIKDMKCIRWESNR | 81 33 SDKALOFPRHLSSGF-R-VDGLEKRSAASESNHYANHLAKQOSEBAFPQEQOKAPPVVGGFNSNGGS 1 | 25 SDKAIQFFRRSSSGF-R-VDGFEKRAAASESNNYAAHVAKQQSEEAFPQEQGRAPPVVGGFNSNVGS 71AFSFSPDFVRPLDRSASSGGE 43 | 163 KYEEIDCLINDE-HTIKGEREGNEVELPFIWVEKYEDVYGKVVQYDCYDREEFSHSYSKVYAGRSP- 1 |
|-------------------------------|---|---|---|---|
| SCORE mouse liver bovine lung | human EST ho Drosophila C. elegans h Methanococcu | SCORE mouse liver | human EST ho Drosophila C. elegans h Methanococcu | SCORE mouse liver bovine lung human EST ho Drosophila C. elegans h Methanococcu |



| 241 January Marie of the Control of | 171 DGVENSFEGYNVEVRURVKCISGVEGVPILSTQNGRQGYFYPIQIAQYGISHYSKNLIEKPPHIEVY | 17 DGVENSFEGINVEVRURVKCISGVEGVPISTOWEPQCYFYPIQIAQYGISHYSKNIJEKPPHIEVY | 163 DGVENSFEGYNVEVRURVRCISGAEGVPILSTQNGRQGYFYPIQIAQYGISHYSKNLIEKPPHIEVY | 168 rgvimtennnvevrorykcisaaegvevstgaekrcyeyptolagealshysknliepapryri | 143 IGPEGHESTYSVETRURVRCVSAKUDVRASTQADPIPYYYPIQISQYGLQHYSRAKUDSISAKSEASPRODVI | 75PINVEEARKCFYKYFKIKYFKIK | 321 state and a second of the | 242 RORNIRBNEWT-VPKGCFNASVADKSRSINVROFIAPETSEGV-SIQICNIROF-IISED | 88 RDKNSKRNUWT-VPKCCFPASVADKSRFINNKQFIAPETSEGV-SLQICNIKOF-IISFD | 234 RDKN-KRNDWT-VPKGCEMANNADKSRETANKQFTARETSEGV-SIQICATKOE-IISED | 236 COCNOM-EWS-TEXTISNMIRIWHERINISWOFETRAPSYECVISIALNOTIDI-11.5ND | 219NSKEWKGAAGMET-TERLFENDEQMEKVVNISAGAALANAGAYVXIDKSEPDIHVISED | 93 -DKNPKEAERYIKRGIFIJEYIISQADKETAETA | 401 E.S | 304 NCSVSVVIETIENXQIFTVHIVSNIQIIAFFORDIYYGIGPRISHSIVI | | | 297 NSSSIMITVQNROIRENYSILEYIPADILILSVQDINIYYG1GSSALNRARHIT | 282 ANSSPTVIAKAKODDIIVIINVYYSEGNAKOMOEEERISDOYIVOKAKOOOVSYSYSYIGNSPIGEWSTVT | 123 -VNERNITFIWR |
|---|---|---|---|--|---|---------------------------|---|--|---|--|---|--|---------------------------------------|---------|---|-------------|--------------|--|---|-------------------------|
| SCORE | mouse liver | bovine lung | human EST ho | Drosophila | C. elegans h | Methanococcu | SCORE | mouse liver | bovine lung | human EST ho | Drosophila | C. elegans h | Methanococcu | SCORE | mouse liver | bovine lung | human EST ho | Drosophila | C. elegans h | Methanococcu |
| | | | | | | | | | | | | | | | - | | | | | |

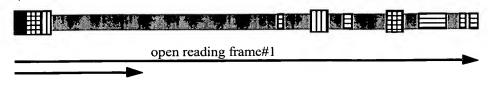


| mouse liver | 328 | 358 DIRKGVGISNTKAVKPTKIMPKKVVRLIAKGKGFIDNITISTTAHMAAFFAASDWIVRNQDEK-G | |
|--------------|-----|---|--|
| bovine lung | 204 | 204 DIRKGVGLSNIKAVKPTRIMPKKVVRLIAKGKGFLDNITISTTAHMAAFFAASDWLVRNQDEK-G | |
| human EST ho | 349 | 349 DIRKGVELSNIKAVKPIKIMPKKVVRLIAKGKGFLDNITISTIAHMAAFFAASDWLVRNQDEK-G | |
| Drosophila | 354 | DLOKGI-MSDKRSPIKIRRSDLEVISIGFLGLGFFDNITLSTSDHLAHFYDAAEMEVHNODPKTG | |
| C. elegans h | 360 | DVARALSSCHNRKKDDNVVLHACDLRLVSLGFRCELTVKOKTTORREOHSHAFYAAADMLVRNONDR-G | |
| Methanococcu | 144 | NLSKG | |
| | | | |
| SCORE | 561 | the self-by self-a L Leide L b. b. be | |
| mouse liver | 425 | IMVIRKLGEGFKSLEPGAVSAMAQGQALSTIJVRAYLLITKDYVFLSSALRATAPYKFPSEQHGYKAV | |
| bovine lung | 271 | IMVIRKLÆGEKSLEPGAVSAMAQGQALSTLVRAYLLIKDHIFINSALRATAPYKFLSEQHGVKAV | |
| human EST ho | 416 | IMVIRKICEGGFKSLEPGAYSAMAQGQAISTLVRAYLLTKDHIFINSALRATAPYKFISEQHGVKAV | |
| Drosophila | 423 | VRRSIN-GFAEIRPGAISAMSQGHAISVIARAYWHSGGDERYIRAAAAGIQPYRVYSRDGGVIAQ | |
| C. elegans h | 433 | VERSIAERKUVI.PPGAHSAMAQGHGISVI.IRAFKHENDEKYI.KSAAKALKI.FKINSSDGGVRGE | |
| Methanococcu | 149 | | |
| | | | |
| SCORE | 641 | | |
| mouse liver | 495 | 495 HDWYEEYPTIPSSFVINGFMYSLIGLYDLKETAGETIGKEARSLYERGMESLKAMLPLYDTGSGT | |
| bovine lung | 341 | | |
| human EST ho | 486 | HDWYEEYPTTPSSFVINGFWYSLIGLYDLKETPACEKLCKEARSLYERCAESLKAMLPLYDTGSCT | |
| Drosophila | 491 | FYWYEEYPTIPPSYVINGFIYSILGLYDINSTAPGKIAREAGKIFAQGMHSIKKMILLFDTGSGT | |
| C. elegans h | 501 | I-WYEEYPTTPGSFVINGFLYSLIGLYDLSQLEIMIDENDETMRAKT-QEAQELYSAGVRSLKQLLPLYDTGSGT | |
| Methanococcu | 205 | YYWFPEYASENPPYVINGFIY | |
| | | | |
| SCORE | 721 | | |
| mouse liver | 565 | 565 HEMIGIAPNIARWDYHTTHINQLQIISTIDESPIFKEFVKRWKSYLKGSRAKHN | |
| bovine lung | 411 | HFMLGIAPNLARWDYHTTHINQIQILSTIDESPIFKEFVKRWKSYLKGSRAKHN | |
| human EST ho | 556 | HEMLGIAPNLARWDYHTTHINQIQILSTIDESPIEKEFVRRWKSYLKGSRAKHN | |
| Drosophila | 561 | HLSLGVAPNLARWDYHATHVNQILILATIDSDPLLAQTAERWKGYMFGRRAKHN | |
| C. elegans h | 579 | HVALGTAFNLARWDYHAVHVYILKWIAGIEKDEVISKTADRWIGYAYGKRAKHN | |
| Methanococcu | 225 | | |



sig seq-TM conserved peptide seq hotspot

hydrophobic and conserved peptide seq. hotspots



Hypothetical orientation, if inserted into golgi

----->cytosol---->lumen cytosol->lumen----

Key:







signal sequence, highly hydrophobic transmembrane (TM) or buried sequence sequence

Hydrophobic transmembrane (TM) most conserved peptide sequence (>50% similarity to C elegans 71.9 KD hypothetical protein; 38% similarity to Methanococcus hypothetical protein). Note: peptide identity between mouse, bovine and human > 95%!



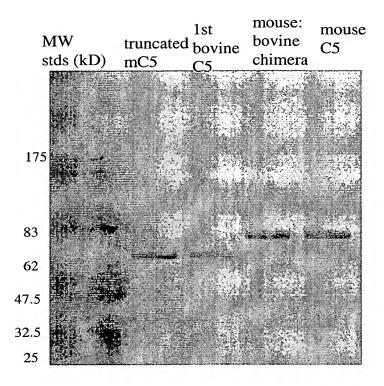


Fig. 9